

sequence 6486 BP; 1600 A; 1559 C; 1687 G; 1639 T; 1 other;

```

conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

22 ccgcggagggcaccaggtggtgccaacaggtgaacatgtacattgtgtcagattactgatct 780

1001 aatctcttctgtatcttcagagagacaaagttaatatcatgtggtccagctgtttt 1920

QY 4081 cctcagatccagaggtccatgtatattctgtttttaaaagaaatlaaaaaataacgg 4140
Db 4081 cctcagatccagaggtccatgtatattctgtttttaaaagaaatlaaaaaataacgg 4140
QY 4141 caatgagagatgagagcccaagaaatacagattcaaaccaaggttttaacaggt 4200
Db 4141 caatgagagatgagagcccaagaaatacagattcaaaccaaggttttaacaggt 4200
QY 4201 ggaacagtgctaaatttggtggtatgcaatgagagaggtgcaaggttcaagaggg 4260
Db 4201 ggaacagtgctaaatttggtggtatgcaatgagagaggtgcaaggttcaagaggg 4260
QY 4261 gccaagagggcccaagcaatcctagatgagagcaagatgcaagaggtctgtgt 4320
Db 4261 gccaagagggcccaagcaatcctagatgagagcaagatgcaagaggtctgtgt 4320
QY 4321 ctggaattctgaaataatttaacctgaaacctgagagcccaatgcatgtgtgtgc 4380
Db 4321 ctggaattctgaaataatttaacctgaaacctgagagcccaatgcatgtgtgtgc 4380
QY 4381 agcccaattgagagagaaacctatcaatgattgagagcccttttctgttccattca 4440
Db 4381 agcccaattgagagagaaacctatcaatgattgagagcccttttctgttccattca 4440
QY 4441 tgaacccagcatcagatgacattgtgagagatgagatgacacccagagagatcttc 4500
Db 4441 tgaacccagcatcagatgacattgtgagagatgagatgacacccagagagatcttc 4500
QY 4501 ctccagagagatgacattgtgagagatgagatgacacccagagagatcttc 4560
Db 4501 ctccagagagatgacattgtgagagatgagatgacacccagagagatcttc 4560
QY 4561 gtaacccagcatcagatgacattgtgagagatgagatgacacccagagagatcttc 4620
Db 4561 gtaacccagcatcagatgacattgtgagagatgagatgacacccagagagatcttc 4620
QY 4621 gtagttctagatgaaag 4680
Db 4621 gtagttctagatgaaag 4680
QY 4681 tggccctggccctctgag 4740
Db 4681 tggccctggccctctgag 4740
QY 4741 aggaag 4800
Db 4741 aggaag 4800
QY 4801 agtggag 4860
Db 4801 agtggag 4860
QY 4861 gcaactgag 4920
Db 4861 gcaactgag 4920
QY 4921 actggaag 4980
Db 4921 actggaag 4980
QY 4981 tggag 5040
Db 4981 tggag 5040
QY 5041 tatgtggag 5100
Db 5041 tatgtggag 5100
QY 5101 ctcttcaagaaag 5160
Db 5101 ctcttcaagaaag 5160

QY 5161 agccaactgtacacctgttccccaagcccttgatgtgagatgagagagagagagagag 5220
Db 5161 agccaactgtacacctgttccccaagcccttgatgtgagatgagagagagagagagag 5220
QY 5221 cccaataag 5280
Db 5221 cccaataag 5280
QY 5281 tgaagaaatttgag 5340
Db 5281 tgaagaaatttgag 5340
QY 5341 gggagatgag 5400
Db 5341 gggagatgag 5400
QY 5401 ctggag 5460
Db 5401 ctggag 5460
QY 5461 ccaagacatgag 5520
Db 5461 ccaagacatgag 5520
QY 5521 gggag 5580
Db 5521 gggag 5580
QY 5581 gggag 5640
Db 5581 gggag 5640
QY 5641 tggag 5700
Db 5641 tggag 5700
QY 5701 cctgag 5760
Db 5701 cctgag 5760
QY 5761 ctgag 5820
Db 5761 ctgag 5820
QY 5821 ctgag 5880
Db 5821 ctgag 5880
QY 5881 agttccctgag 5940
Db 5881 agttccctgag 5940
QY 5941 tttcagaatgag 6000
Db 5941 tttcagaatgag 6000
QY 6001 ccaagacatgag 6060
Db 6001 ccaagacatgag 6060
QY 6061 taag 6120
Db 6061 taag 6120
QY 6121 agttcag 6180
Db 6121 agttcag 6180
QY 6181 ggtcag 6240
Db 6181 ggtcag 6240
QY 6241 tggatag 6300

This sequence represents the retinoblastoma binding protein-7 (RBP-7), genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and probes derived from the RBP-7 nucleotide sequence (e.g., A287035-287036 and A287037-287038) are useful for DNA amplification and detection methods. RBP-7 alleles markers (see A286993-287034) are useful for diagnosis of disease related to alteration in the regulation or in the coding regions of the RBP-7 gene and for prognosis/diagnosis of an eventual treatment with therapeutic agents, especially agents acting on pathologies involving abnormal cell proliferation and/or differentiation, these include thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers, including breast cancer, sarcomas and other neoplasms, bladder cancer, colon cancer, lung cancer, prostate cancer, various leukemias, and lymphomas. RBP-7 antibodies are useful as diagnostic agents.

Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;

Query Match	6.1%	Score 397.67	DB 21:	Length 162450;
Best Local Similarity	58.28%	Pied. No. 7.de-78;		
Matches 1036;	Conservative	0;	Mismatches 68;	Indels 55;
			Gaps	17;
QY	1343	atatccgataatttaaatgcatcttaaggagcgcgcggtggtccacgcgttaatcc	1402	
Db	80674	AAATCAGGCATTAAAAAATATATTTTGGCGGGGTGCATGCTACGCTTAATATCC	80615	
QY	1403	agacatttggaagcccgagatagggtctatcac--gagatcaagagatcgagacatctta	1460	
Db	80614	AGCATTTGGGAGGCGGAGGAGGTGTAATACCTGAATGGGAGACTTGGAGACAGACTG	80555	
QY	1461	gccacaatbagggaacccgcgtctactataaataacaaaaattgcccggaggggttg	1520	
Db	80554	ACCAACATGAGAAAGAACCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	80497	
QY	1521	gaagccctgtagcccaagctatccctccggagagctgagcagagagatbaggcgtgaaccggga	1580	
Db	80496	GGGTGCTCTGTAATCCCACTACTCTGGGAGGCTGTGAGGAGAAATTCCTTGAACCCGGCA	80437	
QY	1581	ggcgaagctgttagtgaagcagagatgacacacgcagcctcagagcttggtggac-aggatg	1639	
Db	80436	GGCAGAGGTGGGGGTGAGCCCAATATTACCCATTGCACTTCAGCCTGTGCACCAAGAGCG	80377	
QY	1640	agactccggtcccaaaaaaaaaa-----aaatgcglttagtctt	1687	
Db	80376	AAATTCATCTCAAAAAATATAAATAATTTTGGAGGCAAAATGCTCTAAACTC	80317	
QY	1688	cgtaaacaaatcaactgcgcctgttggtgttttttggagaagatcgtgctct-gtggagct	1746	
Db	80316	AGTATATACCAACAGAAACTATTTTATTGACGACGAATGTGCAACCCCTATCATTTAGGCT	80257	

[illegible]

Db 14577 tgaactgctggtgctgagctcaagcctgtaaccaaggcacttgaggagctgagtg 14636
 QY 1425 ggccttcac--gagatcaggagatcagagacatccatcagcaacaatggggaacccgctc 1482
 Db 14637 ggtgagatcactgagatccgagagtttgagaccatactgagcaacaatggtggaacccatc 14656
 QY 1483 tctactaaaaatacaaaaaatagccggcgctggtggcggaacccgctgagccagctac 1542
 Db 14697 tctacaaaaatacaaaaaatagctggtggtggcggaacccgctgagccagctac 14756
 QY 1543 tggggagctcagggcagaggaatgagctgaacccggagggagggagctgtgagtcgca 1602
 Db 14757 tggggagctcagggcagaggaatgagctgaacccggagggagggagctgtgagtcgca 14816
 QY 1603 gatcgcacacatgacatccagcctggtgagagagtgagagctcccaaaaaa 1662
 Db 14817 gatcgcacatgacatccagcctggtgagagagtgagagctcccaaaaaa 14876
 QY 1663 aaaaaaaatgcccgttttagt--ctcgttaacaatcactgctgtgtgttttt 1720
 Db 14877 acaacaatgcatctgacttctcctggtgcagagatcaacggtgttttttttt 14936
 QY 1721 tgaagaagctctgctctgtt-----gcggctggagtgacatggtgtgtgtt--g 1769
 Db 14937 tgaagtgtgagttgagctgttttaaccaggtgagagtgagagtgacagatcttgctcg 14996
 QY 1770 ctcaactgacacatccacccctccaggtcgaatgagttatctatccatccagcctccagtag 1829
 Db 14997 ctcaactgacacatccacccctccaggtcgaatgagttatctatccatccagcctccagtag 15056
 QY 1830 ctggtatcaagcgtatcttttttaacgttaatttttttlatcttcaagagagaca 1889
 Db 15057 ccggagttacaggtg--ccggccacatgcccagtgagattttgtatttttagagagagc 15115
 QY 1890 aagagttacatgctgagcagcgtggtttgagacccctgacacatgagatctgcccac 1949
 Db 15116 gta--ttcacatggtgagcagcgtggtctcgacacccctgacacatgagatctgcccac 15174
 QY 1950 ctggtcctcccaagtgctggtgagtaacag--gtgagcacatccgcccagcagttacag 2007
 Db 15175 ctggtcctcccaagtggtgagtaacagcgtgagcagcagcagcagcagcagcagcag 15234
 QY 2008 acaacttaacaatacaacatcttccataaaaaatctc-----aaatggttattca 2061
 Db 15235 ttt 15294
 QY 2062 aaaaaatgtg-----gtagagacatggaagagctttctgtacatca 2105
 Db 15295 agtatagctgagccctgagcaacaatttgagacagagagcctccatgacttccct 15354
 QY 2106 ctataaagcatgcaaaaatgtgagcaaatattttaagttttcaaaagcctgaa 2165
 Db 15355 ctgctcctgacatgctgagatgagcaaccttctctctctctctctctctctctctctc 15414
 QY 2166 agtgttaagagagcactgtaaaatgtggtgagccacatggaagaaagagagagattc 2225
 Db 15415 accggaagatcatgagagagagagacacttattctgtatccacttccatgaatgaagagta 15474
 QY 2226 ctcaaaaaagaatcagggcataatccagcaatgacacttctgtatataac--cagca 2282
 Db 15475 aacataattttctgtctatgacttctcttaataacattttcttctctatattactt 15534
 QY 2283 agactgtgaagccggaacttaagcatgtattcatatcactatgcttcaagcagatcaatt 2342
 Db 15535 atggttaagaatacatatatacaacaatgagacatacaaaaatataatgtaactgtgt 15594
 QY 2343 catactagcnaaaagtggtgagagcccggtgtccatgtatagatgaatgggttaacaa 2402
 Db 15595 tatgtcatgtgaagtctctatattagtttaagttttgagagcnaaaagttatattgt 15654
 QY 2403 caaaaacatgagagattccaccttaaaagtgagacacacaggtgaaacttgaggacatt 2462
 Db 15655 ggcgggtgtgtgtggtcctgtacatccacgaacttgggaggtgaagcaggtgga 15714

QY 2463 atactaaatgaaatgctgcaagctcagagagagagatctctctgtatgagttcaag 2522
 Db 15715 tcaagaggtcaggaatcagagacatccctgtctaaatgagtttaacttcccttactaa 15774
 QY 2523 tggctcatcataaagtgaaatggttaagctgcaaggggctg-----gagggagt 2571
 Db 15775 aatlaaaaaaatagctggtgagctgtgtggtcacacacactgtagccagctactcaagagc 15834
 QY 2572 cgagatgaggaagttaagttagtaacaggtacagagttcaggtttggaagataaag 2631
 Db 15835 tgaagcagggagatcgcttgagaccccggaagcagaggttgcagtgagcagagattgcaat 15894
 QY 2632 tcttgaggtgagatgagtgagcagaggttccacatgtaatgcaatgcaacaatg 2691
 Db 15895 gagcagagagagcagctgacatccagcctgtgtgacagagtgagactctgtctcaaaaaa 15954
 QY 2692 tactcttaaaaaa-----gttgaccgggacaggtgtgctcagcctgaccc 2738
 Db 15955 aaaaaaaataaaaaaaatgtaacccgtcgcgcgggtgagcagcctcaacatgtaac 16014
 QY 2739 cagcacttggtggagcagagcgggagagatcac--aagtgagagatcagagacatcc 2796
 Db 16015 cctactcttggtggagccttaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 16074
 QY 2797 ggtacaacagtgaaaccccgctctactaaatacaaaagaaatgagcgggtggtg 2856
 Db 16075 ggcacaacatgtaaaccccatctactaaatacaaa--aatagttaggtgtgtgt 16131
 QY 2857 gggggtctgtgagctccagctactcgggggtgtgagcagagaaatggttgaacctg 2916
 Db 16132 ggaagcagctgtatccacactcctggtgagagctgagcagagaaatggttgaacccag 16191
 QY 2917 gaggagagctgtgagtgagctgagatccagcactgacatccagcctggtgagagagc 2976
 Db 16192 gaggcagaggtgtgagtgagctgagatccagcactgacatccagcctggtgagagc 16250
 QY 2977 aagactcgtctcaacaacaagaagcaaa 3007
 Db 16251 aagactcgtctcaacaacaagaagcaaa 16281

RESULT 10
 AAI62904
 ID AAI62904 standard; DNA; 32174 BP.
 AC AAI62904;
 XX
 DT 22-Oct-2001 (first entry)
 XX
 DE Human genomic DNA SEQ ID NO 232.
 XX
 KW Human; neotropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antileukemia; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antistickling; antianemic; antidiabetic; cancer;
 KW antileukemic; hepatotropic; cerebroprotective; antileukemia;
 KW antileukemic; antidiabetic; antileukemic; antileukemic; antileukemic;
 KW antiparkinsonian; antileukemic; antileukemic; antileukemic; antileukemic;
 KW neurological disease; infection; immune disorder; cardiovascular disorder;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200155449-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01346.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUL-2000; 2000US-0216880.

PR 14-JUL-2000; 2000US-0218290.
 PR 14-AUG-2000; 2000US-0225447.
 PR 01-SEP-2000; 2000US-0229343.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0231243.
 PR 25-SEP-2000; 2000US-0234997.
 PR 29-SEP-2000; 2000US-0236367.
 PR 13-OCT-2000; 2000US-0239337.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246528.
 PR 17-NOV-2000; 2000US-0248210.
 PR 17-NOV-2000; 2000US-0248211.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249265.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR WPI: 2001-476225/51.
 XX
 PT Novel plasma membrane associated proteins useful for diagnosing,
 PT treating, preventing and/or prognosing disorders related to the
 PT proteins, including cancer, immune response and neuronal disorders
 XX
 PS Example 2; SEQ ID NO 232; 532pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (AI62752-AI62961) and proteins
 CC (AA62347-AA62415) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 XX
 SQ Sequence 32174 BP; 8001 A; 6837 C; 7064 G; 8747 T; 1525 other:

Query Match 5.3%; Score 343; DB 22; Length 32174;
 Best Local Similarity 57.3%; Pred. No. 5,6e-66;
 Matches 981; Conservative 0; Mismatches 655; Indels 75; Gaps 17;

QY 1366 tttagagctggcggcgtgtgctacgcctgtatccca-tgcaattggagagccgaatg 1424
 DB 14577 tgcactgcgtgtgtcagtgctcagcctgtatcccaagcgaattggagagcgtg 14636
 QY 1425 ggtctatcac--gagatcagagatcgcagaccatccagcgaacatggggaacccggt 1482
 DB 14637 ggtgactcacttgatcgcagagatttgagacatcagcgaacatggtggaacccatc 14636

QY 1483 tctactaaataaataaataatagccggcgtgtgtgctgagcgcctgtatcccaagctac 1542
 DB 14697 tctaccataataataaataatagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 14756
 QY 1543 tcggagagctgagcagagagatgtgcgtgaaccggagagcggagagctgtgaatgagccga 1602
 DB 14757 tcggagagctgagcagagagatgtgcgtgaaccggagagcggagagctgtgaatgagccga 14816
 QY 1603 gatgcacacatgcacatccacgcctgggtgacagatgtagtactccgtcccaaaaaaaa 1662
 DB 14817 gatgtgcacatgcacatccacgcctgggtgacagatgtagtactccgtcccaaaaaaaa 14876
 QY 1663 aaaaaaaatgtcctttaggt--cttcgtaaacatcattcagctcgtgtgtgtttt 1720
 DB 14877 acaacaacatcattgatcttctcgtgtgcaggaatcaactgtgtgtgtgtgttttttt 14936
 QY 1721 tgagaagctgtcctgtt-----ggcgctgtagtgcaggtgtgtgtgtgtgt--g 1769
 DB 14937 tgagaagctgtcctgtt-----ggcgctgtagtgcaggtgtgtgtgtgtgtgt--g 14996
 QY 1770 ctcaactcaccctcaccctcccaagctcagtgatctcattgctcagctccagctcagtag 1829
 DB 14997 ctcaactcaccctcaccctcccaagctcagtgatctcattgctcagctccagctcagtag 15056
 QY 1830 ctgtgattacagcagatttttttttaagtaattttttgtattttacagagagaca 1889
 DB 15057 ctgtgattacagcagatttttttttaagtaattttttgtatttttaagtagagagc 15115
 QY 1890 aaagttaatcatgtggtgagcagctgtgttttgaactcctgacatcagtgatccacac 1949
 DB 15116 gta-tttacacatgttgccagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 15174
 QY 1950 ctgtgctcccaagctgt 2007
 DB 15175 ctgtgctcccaagctgt 15234
 QY 2008 acacttaaacatataacacatttctcttaaaaaagctc-----aatgtgtatttca 2061
 DB 15235 ttttttttaattgt 15294
 QY 2062 aaaaatgtgt-----gtagaagacatggaagcttttctgtacataca 2105
 DB 15295 agtatagtgagccttgatcacacacattttgacagcagaggtccctttagcttccct 15354
 QY 2106 ctaataagatgacaaatattgtgtgagcaaatatttttttttcaaaagccttga 2165
 DB 15355 ctgctctgcacgt 15414
 QY 2166 agtgttaatgaggtgacgtgttaaatgtgtgacgacatctgtgaacacagatgagatt 2225
 DB 15415 acctgaagatcatgaggtgaggtgagacattatgtctgacatccatcagatgaagatga 15474
 QY 2226 ctcaaaaaaagaatttcgcgcataatccgaatgcagctcgtgtgtatatacc--caca 2282
 DB 15475 aacatatttttctgtgtatgtatccttcaataaacatttcttctataagttacttt 15534
 QY 2283 agactctgaagcggaaactgaagcagatgtatcatcatcatcagatgtcagcagatcatc 2342
 DB 15535 atgttaagaataatataatataacacaaatgacatacaaaaatatgttaatacaactgt 15594
 QY 2343 catctactgcaaaaaggt 2402
 DB 15595 tatgcatatgt 15654
 QY 2403 cacaacacatgaatcatcacccttaaaagtcaagacacagatgaaactgtgagccatt 2462
 DB 15655 ggcctgt 15714
 QY 2463 atactaatgaaatgtccagtcacaggaagcagagattctctgtatgtatgtatgaag 2522
 DB 15715 tcaagtgatcaggaatcagagacatcctgtgtcaacatgtgtgaattcgtctactaa 15774
 QY 2523 tggctcatcattaaatgtgaatgt 2571

XX	FR2798138-A1.
PN	
PD	09-MAR-2001.
XX	
PF	03-SEP-1999; 99FR-0011097.
PP	
PR	03-SEP-1999; 99FR-0011097.
PS	
PT	(CNRS) CNRS CENT NAT RECH SCI.
PT	Weissenbach J, Hazan J;
XX	WPI; 2001-283966/30.
DR	
XX	
XX	New human nucleic acid from the SPG4 gene, useful e.g. for diagnosis of autosomal dominant familial spastic paraplegia and in drug screening -
XX	Claim 2; Page 45-106; 145pp; French.
CC	
CC	The present sequence represents a human SPG4 gene. The SPG4 gene encodes a spastin polypeptide. Mutations in the SPG4 gene are responsible for autosomal dominant familial spastic paraplegia. SPG4 polynucleotides, CC and their fragments, are used to screen DNA banks for sequences that CC encode spastin (particularly sequences in other mammals, specifically CC mice); to identify SPG4 mutations, or other genetic anomalies, CC particularly for diagnosis of autosomal dominant familial spastic paraplegia (PSP-AD); to identify promoters and other regulatory elements CC of the SPG4 gene; for detection and amplification; for recombinant production of spastin; and for diagnostic genotyping of PSP-AD.
CC	
XX	Sequence 110000 BP; 30622 A; 21640 C; 22817 G; 34921 T; 0 other;
XX	
XX	Query Match 5.2%; Score 338; DB 22; Length 110000;
XX	Best Local Similarity 51.2%; Pred. No. 1.1e-64;
XX	Matches 1458; Conservative 0; Mismatches 1171; Indels 218; Gaps 20.
OY	1371 ggcctggcgcggttgctcaagccctgaatccacgaatttggaggccgagatggcct-1429
Db	95623 GCCACGAGCATGGTGGCTCAGCGCTGTATTCCTTGCACTTAGGAGGCCGAGCGTGCAT 95564
OY	1430 atcccgagatcacgagatcacgagaccactctctgacaatatgggaaaccccgtcttacta 1489
Db	95563 CCCCTGAGGTCAGAGACTTCAGAGACCACCTGGCCACATNAGTAACCCATTCTACTA 95504
OY	1490 aaataac-----aaaaaatagccgggcgtgtgtgtggcgaagccctgtatgccagtta 1541
Db	95503 AAAATATCAAAAAAAAATAAAATTTAGCTGGGGCTGTGGCCATNGCTGTATCTCAGCTA 95444
OY	1542 ctccggagagcttcgagcagaagaaatgcgtcygaaccccggagagcgaagcttgtatgaagcg 1601
Db	95443 CGCAGAGAGGCTTAGGSCAGAGAGATTCGCTTGGAACCTGGAGAGTGAGAGGCTCAGATGACGA 95384
OY	1602 agatcgacacatcatcgaactccaagccttgatgtgacagatgatgacctccgtccaaaataaa 1661
Db	95383 AGATGGTGCCACATCGACATGCAAGCGCTGGGTGACAAGACGAGAAGTCTTCTCAAAAAAAGA 95324
OY	1662 aaaaaaaaaaataagtcggttttagtgccttctgaaaca----- 1696
Db	95323 AATTATTTAAAAAATAAAGTTATTTGAAAAAACAAATATGAAACATTTATTAAGATTTAAC 95264
OY	1697 -----ttaactgcctgtgtgttg 1715
Db	95263 GTATAGTTATAGTTATTTTTTATTTGATATAACCCCCACAAGTTTCATAGTATTTTTTTTT 95204
OY	1716 ttttttgaagaacttgcctctgttgc-----gctcgagatgcacatgcgtgtgatgttggtc 1772
Db	95203 TTTTGAACACGTGGGTCTACCTCCTGTGCCCCAAGCTAAGATGCAATGGGGCAATCTTGCGTC 95144
OY	1773 acgcgaactcacaactcccgagctcaagatgatctcaatgctcctaagctcccgagtaagctt 1832
Db	95143 ACTCAACACCTGTGCTCCCAAGTTCAAGTGAATTCCTCTCCCTCAAGCTCAAGATGACGA 95084

PR 31-AUG-1999: 99UP-0245962.
PR 09-MAY-2000: 2000UP-0136266.

PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.

PI Nakagawa A:
XX WPI: 2001-226686/23.

XX Human 1p36 homozygosity deletion domain from the 36-position of first
XX chromosome short arm in human neuroblastoma cell lines, applicable e.g.
XX in gene diagnosis of tumors as well as in developing anti-cancer drugs

PS Example 8: Page 149-158; 226bp; Japanese.

CC The present invention describes a homozygosity deletion domain
CC co-existing in the 36-position of the first chromosome short arm (1p36)
CC in human neuroblastoma. Also described are base sequences from the 1p36
CC position of human neuroblastoma cell lines (NB-1 and MMS-NB-SCH-1),
CC which are tumour suppressor genes in human neuroblastoma. The genes are
CC tumour suppressor genes, base sequence data of which are applicable as
CC tumour markers and reagents in studying mechanism of tumour body
CC formation, and gene diagnosis of tumours as well as in developing
CC anti-cancer drugs. AAF9787 to AAF97829 represent PCR primers used in
CC the exemplification of the present invention, and AAF97830 to AAF97874
CC represent sequences given in the exemplification of the present
CC invention.

XX Sequence 22081 BP; 5910 A; 5508 C; 5430 G; 5233 T; 0 other:

Query Match 5.1%; Score 328.2; DB 22; Length 22081;
Best Local Similarity 55.3%; Pred. No. 9, 4e-63;
Matches 939; Conservative 0; Mismatches 668; Indels 90; Gaps 12;

QY 1344 tctcggatatttaaatgcttgaaggctggcgcgctgctcagccctgtaatcca 1403
DB 11905 tctcggatataaacaagcagcagctgctggccgggggaagtgtcttcctgtaatcca 11964
QY 1404 gcaatttggaagcgcgaatggtgctatcagatcaagaga-----tcgagacatc 1457
DB 11965 gcaatttggaagcgcgaatggtgctatcagatcaagatcagcgttggaagacagc 12024
QY 1458 ctgagcaaatcggggaacccgctctctactataaatacaaaaattagccggcgctgct 1517
DB 12025 ctgagcaaatcggggaacccgctctctactataaatacaaaaattagctggcgctg 12084
QY 1518 ggcgagcgcctgtatgccagctactcgggagcttgagcagagag--aatggcgtgaac 1575
DB 12085 ggcagctgcccgtgaacccagcagctcgggagcttgagcagagagagagagagagc 12144
QY 1576 cggagagcgaagctgtgagcagcagatcgcacacccatcctcagcctgggtgagc 1635
DB 12145 ggggaggttaaaagtgtgagcagctgtgtaatcactcactcagcctggcgcaagag 12204
QY 1636 agtgaagactcgcgtcccaaaaaa-----aaaaaaaatggcgttta 1681
DB 12205 caagaccagctctaaaaaaaccccaactgctccagggttccagggttcagcaactc 12264
QY 1682 ggtcttcgtaacaattactgctgtttgtttgttttttttttttttttttttttttt 1739
DB 12265 aatggtagtaattgtgtccactatcttttttttttttttttttttttttttttttt 12324
QY 1740 -tggagctgagatgactggtgtgatgtgtgactgactgactcactcactcagagctca 1798
DB 12325 ccgaagcttggaatcagatggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 12384
QY 1799 agtatattcctcagctcagcctcccgatgactgtgattacagcgatttttttttttttt 1858
DB 12385 agcagctccctcagcctcagcctgcaactagctgagatcaggtgtgtgacactgccc 12444

QY 1859 ttaatt 1918
DB 12445 cagctaatctt---ttatt 12501
QY 1919 ttgaaccctgacttcaatgattgtctgctccttcgctcccaagatgtctgtgatacag 1978
DB 12502 tcaagctccctggctcagcagctccctcagcctcagcctcagcctcagcctcagc 12561
QY 1979 -gtgagccactcgcagcagcagcttgcacttcaacaatacaatacatttccctaa 2037
DB 12562 tgtgagccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 12618
QY 2038 aaaaagtccaatgatttatttcaaaaatggtgtgagagacatgtgaaagcctttctg 2097
DB 12619 gcactgctcactctccctctgctgtatccccaagatgacctcagcagcagcagcag 12678
QY 2098 tacatacactaaataagcatgcaaaaattgtgagcaataatttttttttttttttt 2157
DB 12679 attccacttttcaaatga--gaaactggaacacagatagtaataatttcccaag 12737
QY 2158 cctgaaaagtgtaatgagagagcagctgtaaaaatgtgtgcaaccactatgaaacagag 2217
DB 12738 tctaacagctagtaagcaagggcgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 12797
QY 2218 gagagatttccaataaagaattacagcacaatccagcaatgccaactcgtgatatatc 2277
DB 12798 ttggaagtgtaagcggaaagggcgtgagtgatctcctctgacatcactgtttgaac 12857
QY 2278 ccacaagactctgaaagcggaaactgaagcatgfatcatcatcatcatcatcatcat 2337
DB 12858 atcgtgggcctcttgacacttagcctctgacactctgtc----- 12896
QY 2338 tcaatcactcagcacaagagtggtgagcagcccgctgtcacttgatagatgagtgatga 2397
DB 12897 -gtctctccatccatccagcagtgctccatccctcagctcagcagcagtgaaagatc 12954
QY 2398 aacaacacaaacatgaatgatttccactttaaagtacagacacagatgaacttgagag 2457
DB 12955 cccctcagcagtgctcttgacacagctttaaagaaaalcccgtaacgttggctactcg 13014
QY 2458 ccaattacttaataatgaatgatcagctcagctcagcagcagcagcagcagcagcagc 2517
DB 13015 gactcctcttaatgta-----cagggagtgcaaggggtgtgtgtgtgtgtgtgtgt 13068
QY 2518 cagagtgctcactatcaatgaatgagtgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2577
DB 13069 cgaagtaactcactcagctagcagagtttaaaagtgtgtgtgtgtgtgtgtgtgtgt 13128
QY 2578 tgggaagttaatgttgaacagcagtgagctcagcttgggaagataaaagtgtgtgt 2637
DB 13129 ctataatccagcagccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 13188
QY 2638 aggtgtgagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2697
DB 13189 catcagcctgtggtc-----atcataagaaagacacatct 13221
QY 2698 taanaacagcttgacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2756
DB 13222 ctatacaaaattttaaataatcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 13281
QY 2757 agcggcgagatcacaaggtcagagagatcagacatcctgtgtgtgtgtgtgtgtgtgt 2816
DB 13282 aggt 13341
QY 2817 gtctcactaataataaagaatgagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2876
DB 13342 gtctcactaataataaataaagaatgagcagctgtgtgtgtgtgtgtgtgtgtgtgtgt 13401
QY 2877 ctctcgt 2936
DB 13402 ctctcgt 13461
QY 2937 ctgagatccagcactgacactcagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2996

Fri Nov 30 11:03:15 2001

us-09-526-329-40.rng

Page 20

Db 13462 ccaagaccacgcccactgactccagccttggatgacagagcagactctgtctcaaaaaa 13521
Qy 2997 acaagcaaaacaaaa 3013
Db 13522 agaaaaataattaaaa 13538

Search completed: November 29, 2001, 09:34:35
Job time: 19671 sec

Db 13113 TTTTCTTTTGTGAGACGGAGTCTACCTCTGTCCCGACGGATGGATGGATGGTGGGA 13054

Qy 1764 tgttggtctaacgcgaactccactccactccaggctcaagtgatcttcagctcgaagctccc 1823

Db 13053 GCTAGCTCACTGCAACCTCCACCTCCGGGTTACGCCATCTCTCGCTCAAGCTGCC 12994

Qy 1824 gagtagcttggattacaagcgatttttttaacagtaattttttgttattttcaaga 1883

Db 12993 GAGTAGCTGGGACTCTACAGGGCCCCCACACCAACCAAGCTAATTTTTTGTATTTTAACTA 12934

Qy 1884 gagacaaagttaatactcgtggtggccagctcgtgttgaacaccctgaaccctcaagtaacct 1943

Db 12933 GAGAC -GGGTTTCAACGCTGTGACAGGATGTCCTGATCTCTGACATC -GIGATCC 12877

Qy 1944 gccacacttggctcccaaaagtccttggattacag -gtgaacacacctgcgcgcacagc 1998

Db 12876 ACCCACTCCACCTCCCAAAAGTCTGGAGTTTACAGCGTGTGACCAACGCGCCCGGGCC 12820

```

RESULT      3
US-08-781-891-79
Sequence 79, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRI LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620lenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-79

Query Match      4.8%; Score 309.4; DB 3; Length 87350;
Best Local Similarity 72.6%; Pred. No. 3,46-71;
Matches 480; Conservative 0; Mismatches 145; Indels 36; Gaps 5;

```

OY	1416	gcgcagagtagcttatacagaagatcaggaatcgaacacactgaacaaatgaggaaa	1475
Db	29563	gccacagccggcgcatcaccagattgagaaatgcacgcatctccgcttaacacgttmaa	29622
OY	1476	cccgcctcactaaataataaaaaattagccggcgctggtgtagcggaecgctgagtc	1535
Db	29623	ccccgtttctactataaaatcAAAAAATTAACCGGGCGCGTGGTGGCGGGTCTGTAATCC	29682
OY	1536	cagcactctgggaagctcgaagcagaggaatgctgaacccggagagcgaaagcttgagtt	1595
Db	29683	caggttacttggcggcctgagcagcaggaatggcgtgaacccggagcgagacttgcagc	29742
OY	1596	gagccggagatgcaccactgcaatcgaacctgggtgaacaggttagagctcggctccaaa	1655
Db	29743	gagcggagatccggcgcactgcactccagctgggtgacaggttagagctcggctccaaa	29802
OY	1656	aaaaaanaaaaaaanaa-----tgcgtttagttcctcgt	1690
Db	29803	AAAAATTAATAATAATAATAATAATTTCTAGACCACTACTTATGAGAGCGTGTTTT	29862
OY	1691	aaacaattcaactgcgtgtgtgtgtgtgtgttttttgagaagctcgtgcctgtg-----cgg	1744
Db	29863	tgtttttttttgtgttt	29922
OY	1745	ctgagagtcgaactgctgtagatgtt--ggtcaactgcaactccactcccaagctcaagt	1802
Db	29923	ctagagctgacagttggcgcatctccnccgctcactccaaactccggctctctgggtttaaagcc	29982
OY	1803	attccatgcctcaagcctcccgagtagcttgattcaagcgatcttttttttacagttaa	1862
Db	29983	atttcctccgctcagcctcccgaaatagctgggaattacagtttgcggctggcacaaccccgcc	30042
OY	1863	ctttttttgttatcttcagagagacaaaagttaatcatctgtggtggccgaagctggtttga	1922
Db	30043	TAAATTTTGTATTTT--AGTAAGATGATGGATTCACATGTTGTTCCAGGCGTGGTGTGA	30100
OY	1923	acctctgcaactcaatgtagctgcgcacactctggcctcccaaaagtctgagattacagttga	1982
Db	30101	actcctgagctcagcgaatccaccgcccccggcctcccaaaattgtggatattacagcgt	30160
OY	1983	g 1983	
Db	30161	G 30161	

RESULT 4
 US-08-814-095-7/C
 ; Sequence 7, Application US/08814095
 ; Patent No. 6025183
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Soreq, Hermona
 ; APPLICANT: Soreq, Haim
 ; APPLICANT: Shani, Moshe
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
 ; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
 ;
 ; NUMBER OF SEQUENCES: 7
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: KOHN & ASSOCIATES
 ; STREET: 30500 NO. 6025183Western Highway, Suite 410
 ; CITY: Farmington Hills
 ; STATE: Michigan
 ; COUNTRY: U.S.
 ;
 ; ZIP: 48334
 ;
 ; COMPUTER READABLE FORM:
 ;
 ; MEDIUM TYPE: floppy disk
 ;
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ;
 ; CURRENT APPLICATION DATA:
 ;
 ; APPLICATION NUMBER: US/08/814, 095
 ;
 ; FILING DATE:
 ;
 ; CLASSIFICATION: 800
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ;

NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.00066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid including ACH
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
FEATURE:
NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACH Promotor"
OTHER INFORMATION: /standard_name= "ACH Promotor"
FEATURE:
NAME/KEY: exon
LOCATION: 22465..22537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: 24090..25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translacion start:
OTHER INFORMATION: 24110)"
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 3
FEATURE:
NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: 27255..28007
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 5
FEATURE:
NAME/KEY: terminator
LOCATION: 27385..27387
FEATURE:
NAME/KEY: exon
LOCATION: 28008..28129
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
FEATURE:

NAME/KEY: terminator
LOCATION: 28129..28131
FEATURE:
NAME/KEY: exon
LOCATION: complement (34528..34895)
OTHER INFORMATION: /function= "arsenite resistance
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 1
FEATURE:
NAME/KEY: exon
LOCATION: complement (34092..34358)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 2
FEATURE:
NAME/KEY: exon
LOCATION: complement (33779..33963)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
FEATURE:
NAME/KEY: exon
LOCATION: complement (33493..33591)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
FEATURE:
NAME/KEY: exon
LOCATION: complement (33297..33408)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
FEATURE:
NAME/KEY: exon
LOCATION: complement (32959..33094)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
FEATURE:
NAME/KEY: exon
LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
FEATURE:
NAME/KEY: exon
LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
FEATURE:
NAME/KEY: exon
LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
FEATURE:
NAME/KEY: exon
LOCATION: complement (31363..31534)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
FEATURE:
NAME/KEY: exon
LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
FEATURE:
NAME/KEY: exon
LOCATION: complement (30816..31011)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
FEATURE:
NAME/KEY: exon
LOCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
FEATURE:
NAME/KEY: exon
LOCATION: complement (30187..30274)
OTHER INFORMATION: /gene= "AR"


```

1 OTHER INFORMATION: /number= 5
2 FEATURE: terminator
3 NAME/KEY: terminator
4 LOCATION: 27385..27387
5
6 FEATURE:
7 NAME/KEY: exon
8 LOCATION: 28008..28129
9 IDENTIFICATION METHOD: experimental
10 OTHER INFORMATION: /evidence= EXPERIMENTAL
11 OTHER INFORMATION: /gene= "ACHE"
12 OTHER INFORMATION: /number= 6
13
14 FEATURE:
15 NAME/KEY: terminator
16 LOCATION: 28129..28131
17
18 FEATURE:
19 NAME/KEY: exon
20 LOCATION: complement (34528..34895)
21 OTHER INFORMATION: /function= "arsenite resistance"
22 OTHER INFORMATION: /gene= "AR"
23 OTHER INFORMATION: /gene= "AR"
24 OTHER INFORMATION: /number= 1
25
26 FEATURE:
27 NAME/KEY: exon
28 LOCATION: complement (34092..34358)
29 OTHER INFORMATION: /gene= "AR"
30 OTHER INFORMATION: /number= 2
31
32 FEATURE:
33 NAME/KEY: exon
34 LOCATION: complement (33779..33963)
35 OTHER INFORMATION: /gene= "AR"
36 OTHER INFORMATION: /number= 3
37
38 FEATURE:
39 NAME/KEY: exon
40 LOCATION: complement (33493..33591)
41 OTHER INFORMATION: /gene= "AR"
42 OTHER INFORMATION: /number= 4
43
44 FEATURE:
45 NAME/KEY: exon
46 LOCATION: complement (33297..33408)
47 OTHER INFORMATION: /gene= "AR"
48 OTHER INFORMATION: /number= 5
49
50 FEATURE:
51 NAME/KEY: exon
52 LOCATION: complement (32959..33094)
53 OTHER INFORMATION: /gene= "AR"
54 OTHER INFORMATION: /number= 6
55
56 FEATURE:
57 NAME/KEY: exon
58 LOCATION: complement (32569..32628)
59 OTHER INFORMATION: /gene= "AR"
60 OTHER INFORMATION: /number= 7
61
62 FEATURE:
63 NAME/KEY: exon
64 LOCATION: complement (32386..32468)
65 OTHER INFORMATION: /gene= "AR"
66 OTHER INFORMATION: /number= 8
67
68 FEATURE:
69 NAME/KEY: exon
70 LOCATION: complement (31894..32080)
71 OTHER INFORMATION: /gene= "AR"
72 OTHER INFORMATION: /number= 9
73
74 FEATURE:
75 NAME/KEY: exon
76 LOCATION: complement (31363..31534)
77 OTHER INFORMATION: /gene= "AR"
78 OTHER INFORMATION: /number= 10
79
80 FEATURE:
81 NAME/KEY: exon
82 LOCATION: complement (31131..31284)
83 OTHER INFORMATION: /gene= "AR"
84 OTHER INFORMATION: /number= 11
85
86 FEATURE:
87 NAME/KEY: exon

```

[illegible]

Db 3153 CCAGCTACTTGGAGGCTGAGGACAGAGAAATGGCGTGAACCCGGAGCGGAGCTTGACG 3212

Qy 1595 TGAGCGAGATGCGACCACTGCACTGAGTGTGACAGAGTGAAGTCCGCTCCGCAAA 1654

Db 3213 TGAGCCGAGATGCCGCACTGCACTGAGTGTGACAGAGTGAAGTCCGCTCCGCAAA 3272

Qy 1655 aaaaaaaaaaaaaa 1672

Db 3273 AAAAAAAAAAAAAAAAAA 3290

RESULT 8

US-08-724-394A-21

; Sequence 21, Application US/08724394A

; Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Krommal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

TITLE OF INVENTION: Sequences and Antibodies Thereo

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0200

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H. CONTIG"

US-08-724-394A-21

Query Match 4.2%; Score 270; DB 2; Length 246240;

Best Local Similarity 90.6%; Pred. No. 2, le-60;

Matches 288; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 1355 ttaaatgcatltaggctggcgctgagctgagctgtaattccagcaacttggga 1414

Db 2973 TAAAGAGCTTTATTAAGCGCGCGGCGGTCTACCGCTGAATCCAGCAGCATTTGGGA 3032

Qy 1415 ggcgcgagatgggtatcacgagatcagagatcgaacatccctgcaacatgggaa 1474

Db 3033 GGCCGAGCGGCGGATCAGGATCAGAGATCCGCGCTAAACGGTGAA 3092

Qy 1475 accgcgtctcttaaaatacaaaataaagcggcggtgagcgagcgctgtatc 1534

Db 3093 ACCCGCTCTTACTTAAATATCAAAAATTTAGCGGCGGTGTGAGTGTGATGTC 3152

Qy 1535 ccagctactcggagagctgagcgagagatgagctgaaaccggagagcgagctgtag 1594

Db 3153 CCAGCTACTTGGAGGCTGAGGACAGAGAAATGGCGTGAACCCGGAGCGGAGCTTGACG 3212

Qy 1595 TGAGCGAGATGCGACCACTGCACTGAGTGTGACAGAGTGAAGTCCGCTCCGCAAA 1654

Db 3213 TGAGCCGAGATGCCGCACTGCACTGAGTGTGACAGAGTGAAGTCCGCTCCGCAAA 3272

Qy 1655 aaaaaaaaaaaaaa 1672

Db 3273 AAAAAAAAAAAAAAAAAA 3290

RESULT 9

US-08-724-394A-22

; Sequence 22, Application US/08724394A

; Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Krommal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

TITLE OF INVENTION: Sequences and Antibodies Thereo

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 017957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 246240 base pairs

TYPE: nucleic acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..246240

OTHER INFORMATION: /note= "HLA-H. CONTIG"

US-08-724-394A-22

Query Match 4.2%; Score 270; DB 2; Length 246240;

Best Local Similarity 90.6%; Pred. No. 2, le-60;

Matches 288; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1355 ttaaatgcaattagagctgagcgagtgagctacagccgtatccagactttgga 1414
 Db 2973 TATAAAGCTTTATATAGCGCGCGCGGTGCTCAGCCCTGTAATCCAGACTTTGGGA 3032
 QY 1415 ggcgcgagatggctatcagagatcagagatcagaccatccagcaaatgggaa 1474
 Db 3033 GGGCGAGGCGCGGCGATCAGAGAGTCAGAGATCGAGACCTCCGGCTAAAGGGTGA 3092
 QY 1475 acccgctctactaaataacaaaattagccgagcgctgggtgagcagcctgtatgc 1534
 Db 3093 ACCCGCTCTACTAAATAATACAAAAATAGCCGGGCGCTAGTGGCGGCGCTGTAGTC 3152
 QY 1535 ccagctactcgagagctgagcgagagagatgagctgaaacccggagagcaaatgttg 1594
 Db 3153 CCAGCTACTTGGAGGCTGAGGCGAGAGAAATGCGGTGAACCCGGGAGCGAGCTTGCA 3212
 QY 1595 tgaagcgagatcgacacactgcactccagcctgggtgagagagtgagactccgcca 1654
 Db 3213 TAGCGCGAGATCCCGCACTGCATCCAGCTGGCGGAGAGCAAGACTCCGTCAAA 3272
 QY 1655 aaaaaaaaaaaaaaa 1672
 Db 3273 AAAAAAAAAAAAAAAAAA 3290

RESULT 10

US-08-94-915-5
 ; Sequence 5, Application US/08694915
 ; Patent No. 5811535
 ; GENERAL INFORMATION:
 ; APPLICANT: Adamou, Julie
 ; APPLICANT: Kirkpatrick, Robert
 ; APPLICANT: Rosenberg, Martin
 ; TITLE OF INVENTION: HUMAN CARTILAGE GP39-LIKE GENE
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/694,915
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Han, William T
 ; REGISTRATION NUMBER: 34,344
 ; REFERENCE/DOCKET NUMBER: ATG50017
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5219
 ; TELEFAX: 610-270-5090
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3742 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO

; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; US-08-694-915-5

Query Match 4.1%; Score 268.2; DB 1; Length 3742;
 Best Local Similarity 89.7%; Pred. No. 3,9e-61;
 Matches 288; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 1356 taaatgcaattagagctgagcgagtgagctacagccgtatccagactttgga 1415
 Db 2307 TATAAAGAAACACAGCGCGCGCGGTGCTCAGCCCTGTAATCCAGACTTTGGAG 2366
 QY 1416 ggcgcgagatggctatcagagatcagagatcagaccatccagcaaatgggaa 1475
 Db 2367 GCGGAGGCGCGGCGATCAGAGAGTCAGAGATCGAGACCTCCGGCTAAAGGGTGA 2426
 QY 1476 cccgctctactaaataacaaaattagccgagcgctgggtgagcagcctgtatgc 1535
 Db 2427 CCCGCTCTACTAAATAATACAAAAATAGCCGGGCGCTAGTGGCGGCGCTGTAGTC 2486
 QY 1536 ccagctactcgagagctgagcgagagagatgagctgaaacccggagagcaaatgttg 1595
 Db 2487 CAGCTACTTGGAGGCTGAGGCGAGAGAAATGCGGTGAACCCGGGAGCGAGCTTGCA 2546
 QY 1596 gagcgagatcgacacactgcactccagcctgggtgagagagtgagactccgcca 1655
 Db 2547 GAGCGAGATCACACCACTGCATCCAGCTGGCGGAGAGCAAGACTCCGTCAAA 2606
 QY 1656 aaaaaaaaaaaaaatgcc 1676
 Db 2607 AAAAAAAAAAAAAAAAAAAGAAC 2627

RESULT 11

US-08-629-939-5/c
 ; Sequence 5, Application US/08629939
 ; Patent No. 5645995
 ; GENERAL INFORMATION:
 ; APPLICANT: Kieback, Dirk G.
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED
 ; TITLE OF INVENTION: RISK OF BREAST OR OVARIAN CANCER
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 ; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
 ; CITY: Washington, D.C.
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/629,939
 ; FILING DATE: 12-APRIL-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KIT, Gordon
 ; REGISTRATION NUMBER: 30,764
 ; REFERENCE/DOCKET NUMBER: A-6612
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 293-7060
 ; TELEFAX: (202) 293-7860
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 320 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA

US-08-629-939-5

Query Match	4.1%	Score 268;	DB 1;	Length 320;
Best Local Similarity	90.5%	Pred. No. 8.7e-62;		
Matches 286; Conservative	0;	Mismatches 30;	Indels 0;	Gaps 0;

QY	1357	aaatgcattatlagagctcygacggttgctaacctcgtaatccoaagactttggagag	1416
Db	320	AAAAATGTTTTCGGGGCGGGCGGGGTGAGCTGTAACTCCACACTTTGGGAGG	261
QY	1417	ccgagatcgggctataccaagatcagagatctgagaccatctagacaatcagggaaac	1476
Db	260	CCGAGCGGGCGGGATACGAGAGTCCAGAAATGGAACATCTGGCTTAAACGGGTAAAC	201
QY	1477	ccgctctcctactaaatacacaaaaatctagccggcgctggctgagcaagcctgtatccc	1536
Db	200	CCCGCTCTCTATAAAAAATTAACAAAAATTAGCTGGGCGCTAGTGGCGGGCGCTGATGCC	141
QY	1537	agctaccgcgggaggtctggggaaggaatacgcgtgaaacccgggagggcgaagctttgagt	1506
Db	140	AGCTACTTGGGAGGCTGAGGAGGGAATAAGGGGTGAACCCGGAGAGCGGAATCTGAGTGC	81
QY	1597	agccgagatcgcacacactgcactccagcctcgtgtgaaagatctgagactcgcgtcccaaaa	1656
Db	80	AGCCGAAATCCGCGACACTGCACCTGACCTGGGCGACAGCGACAGCTCGTCTCAAAAA	21
QY	1657	aaaaaaaaaaaaaaaaa 1672	
Db	20	AAAAAAAAAAAAA 5	

RESULT 12
US-08-759-

Sequence 5, Application US/08759873
Patent No. 5683885
GENERAL INFORMATION:
APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRE, MIOM, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
CITY: Washington, D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,873
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO

US-08-759-873-5

Query Match	4.18;	Score 268;	DB 1;	Length 320;
Best Local Similarity	90.5%;	Pred. No. 8.7e-62;		
Matches 286;	Conservative	0;	Mismatches 30;	Indels 0;
			Gaps	0;

QY	1357	aaatgacattttagggcctgagcgcggtgagctaacgctgaatcccaacatttggag	1416
Db	320	AAAAATGTTTTTGCGGCGGCGGGGCGCTCAGCCGTGAATCCAGACTTTGGNAG	261
QY	1417	ccggatagggtctatcaagaaataggaatctgagaccatctagccaacttgggaac	1476
Db	260	CGAGGCGGCGGATGTCGGAAGTGAAGAAATGAACCATCTCGCTAAACGGGTAAAC	201
QY	1477	ccgctctctactaaataacaaaanaattagccggcgcttggttgcgagacgctgtgcc	1536
Db	200	CCCGCTCTCTATAAAAAATACAAAAAATATAGCTGGGCGCTAGTGGCGGCGCTGATGCC	141
QY	1537	agctaccctggagagctggaggaagaaatagctgaaaccctggagaggaacttgcagtg	1596
Db	140	AGCTTACTTTGGGAGGCTGAGGAGAGAAATGGGCTGAACCCGGGAGGCGGAACTTGGCAGTG	81
QY	1597	agccgagatctgcaccactgtcacctccagccttgggtgaaagatgtagactcgtcccaaaa	1656
Db	80	AGCCGAGATCCGCCACATGCACCTCCAGCTGGGCGACAGAGCCAGACTCCTGCTCAAAA	21
QY	1657	aaaaaaaaaaaaaaaaa	1672
Db	20	AAAAAAAAAAAAAAAAA	5

RESULT 13

```

US-09-173-914-6/c
? Sequence 6, Application US/09173914
? Patent No. 6171857
? GENERAL INFORMATION:
? APPLICANT: Hendrickson, Eric
? TITLE OF INVENTION: A No. 6171857el launcing zipper, KRP-1 and
? TITLE OF INVENTION: Methods of Regulating DNA Dependent Protein Kinase Activity
? FILE REFERENCE: B0877/7/017/HK
? CURRENT APPLICATION NUMBER: US/09/173, 914
? CURRENT FILING DATE: 1998-10-16
? EARLIER APPLICATION NUMBER: 60/064,557
? EARLIER FILING DATE: 1997-10-17
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: FastSeq For Windows Version 3.0
? SEQ ID NO 6
? LENGTH: 14636
? TYPE: DNA
? ORGANISM: Homo Sapiens
? US-09-173-914-6

```

Query Match	4.1%;	Score 264.6;	DB 4;	Length 14636;
Best Local Similarity	92.1%;	Pred. No. 8.7e-60;		
Matches 279;	Conservative	0;	Mismatches 24;	Indels 0;
				Gaps 0;

QY	1370	ggagctggccgcggtgtgtccacgcgcctgatacccgaacttggagagccgaatggttc	1429
Db	12534	ggggccggccggccggtgctctacacctgtatattccacgacttggagagccgaatggttc	1429
QY	1430	atcacgagatactcgagagatactcgagacatactcttcgccaacatgggagaaacccgcgtctacta	1489
Db	12474	atcagcgaggtcagagagatcgagaccatctccggcgtaaaagggtaaaccttgcctctacta	1415
QY	1490	aaaatacaaaaatctagcgcgggcgtgtgtgtgcgagacgcgtctagatccagctactccggag	1549
Db	12414	aaaatacaaaaatattacccggcggtgtagtggcgggccgctgtagtccacgactcttggagag	1549
QY	1550	gctbgaagcagagaaatggcgttgaaaccggggagggcgagagcttgtagagcgcagatgcga	1609
Db	12354	gctbgaagcagagaaatggcgttgaaaccggcgagggagggcgttgacagatgcgaagatgcga	1609

QY 1610 ccactgactccagcctgtgtgacagatgagctccgcccaaaaaaaaaaaaaa 1669
 |||
 Db 12234 CCACTGCACCTCCAGCCTGGGCGACAGAGAGACTCGCTCCCAAAAAAAAAAAAAA 12235

QY 1670 aaa 1672
 |||
 Db 12234 AAA 12232

RESULT 14

US-08-975-080-35
 ; Sequence 35, Application US/08975080
 ; Patent No. 6245523
 ; GENERAL INFORMATION:
 ; APPLICANT: Altierl, Dario C.
 ; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 ; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 ; STREET: 1800 M Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20036-5869
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/975,080
 ; FILING DATE: 20-NOV-1997
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/031,435
 ; FILING DATE: 20-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Adler, Reid G.
 ; REGISTRATION NUMBER: 30,988
 ; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-467-7000
 ; TELEFAX: 202-467-7176
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14796 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-975-080-35

Query Match 4.1%; Score 263; DB 4; Length 14796;
 Best Local Similarity 90.4%; Pred. No. 2.3e-59;

Matches 281; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1357 aaatgacatttagagcgtgagcgagcgtgacacccgtgtaacccgagacttggagag 1416
 |||
 Db 8623 AAGTAGACTTTCAGGCGCGGATGAGTCAAGCCTGTATATCCAGCACTTTGGAGG 8662

QY 1417 ccgagatgagcttatacagagatcagagagacatccatctagccaacatgggaaac 1476
 |||
 Db 8683 CCGAGGCGGCTGATCAGAGAGTCAAGATCCATCTGCTAACAATGCGAANAC 8742

QY 1477 ccgctctctactaataatacaaaaaattagccggcgctgctgagcgagcctgtatgcc 1536
 |||
 Db 8743 CCGCTCTTTACTTAATAATACAAAAATTACCTGGCGGTGAGCGGCGCCTGTAGTCCC 8802

QY 1537 agctactcggagagcgtgagcagagaatgagcgtgacccggagcgagcgtgtagtg 1596
 |||
 Db 8803 AGCTACTCGGAGCGCTGAGCGAGAGATGCGGTGAACCTGGAGGTGAGCTTCTGTG 8862

QY 1597 agccgagatcgaccactgacactccagcctgtgtgacagatgagactccgccaaaaa 1656
 |||
 Db 8863 AGCGAGATCGGCGCACACTGCACAGCTGGGCGACAGAGAGACTCGCTCCAAAAA 8922

QY 1657 aaaaaaaaaa 1667
 |||
 Db 8923 AAAAAAAAAA 8933

RESULT 15

US-09-630-706-10
 ; Sequence 10, Application US/09630706
 ; Patent No. 6277640
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Lex M. Cowsett
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF HBR-3 EXPRESSION
 ; FILE REFERENCE: RTS-0053
 ; CURRENT APPLICATION NUMBER: US/09/630,706
 ; CURRENT FILING DATE: 2000-08-01
 ; NUMBER OF SEQ ID NOS: 94
 ; SEQ ID NO 10
 ; LENGTH: 14796
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (2811)...(2921)
 ; NAME/KEY: CDS
 ; LOCATION: (3174)...(3283)
 ; NAME/KEY: CDS
 ; LOCATION: (5158)...(5275)
 ; NAME/KEY: CDS
 ; LOCATION: (11955)...(12044)
 ; US-09-630-706-10

Query Match 4.1%; Score 263; DB 4; Length 14796;
 Best Local Similarity 90.4%; Pred. No. 2.3e-59;

Matches 281; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1357 aaatgacatttagagcgtgagcgagcgtgacacccgtgtaacccgagacttggagag 1416
 |||
 Db 8623 AAGTAGACTTTCAGGCGCGGATGAGTCAAGCCTGTATATCCAGCACTTTGGAGG 8682

QY 1417 ccgagatgagcttatacagagatcagagagacatccatctagccaacatgggaaac 1476
 |||
 Db 8683 CCGAGGCGGCTGATCAGAGAGTCAAGATCCATCTGCTAACAATGCGAANAC 8742

QY 1477 ccgctctctactaataatacaaaaaattagccggcgctgctgagcgagcctgtatgcc 1536
 |||
 Db 8743 CCGCTCTTACTTAATAATACAAAAATTAGCCTGTATATCCAGCACTTTGGAGG 8802

QY 1537 agctactcggagagcgtgagcagagaatgagcgtgtaacccggagcgagcgtgtagtg 1596
 |||
 Db 8803 AGCTACTCGGAGCGCTGAGCGAGAGATGCGGTGAACCTGGAGGTGAGCTTCTGTG 8862

QY 1597 agccgagatcgaccactgacactccagcctgtgtgacagatgagactccgccaaaaa 1656
 |||
 Db 8863 AGCGAGATCGGCGCACACTGCACAGCTGGGCGACAGAGAGACTCGCTCCAAAAA 8922

QY 1657 aaaaaaaaaa 1667
 |||
 Db 8923 AAAAAAAAAA 8933

Search completed: November 29, 2001, 09:31:09
 Job time: 19465 sec

Fri Nov 30 11:03:16 2001

us-09-526-329-40.rni

Page 13

Db 57 GACCTGACAGTACCTGCTTAATTAACCTTATTCCTC 21

RESULT 3
AM575965/c 495 bp mRNA EST 15-MAR-2000
LOCUS UI-HF-BL0-acu-h-03-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3059932 3', mRNA sequence.
ACCESSION AM575965
VERSION AM575965.1 GI:7247420
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 495)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbrrp/image/image.html
Seq primer: M13 Forward
POLYA-Yes

FEATURES

Source 1..495
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3059932"
/clone_1bp="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (RTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic RNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 124 a 131 c 129 g 109 t 2 others
ORIGIN

Query Match 7.3%; Score 476.4; DB 10; Length 495;
Best Local Similarity 99.4%; Pred. No. 3; 8e-48;
Matches 477; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 5854 actgagccctgctgtgctgagccagcttccctctgctgagccagctgtggtct 5913
|||||
Db 495 ACTGGGGCCCTGCTGTGCTGAGCCAGTTCCCTGCTGCTGCAAGCTGGGGTCT 436
|||||
Db 5914 ttctctctgtgcccctcctcgtatctctatagatgcaatccctccctatacc 5973
|||||
Db 435 TTCTCTCTGTGCCCCCTCATGCTGATTTTTFATAGTCCACATCCCAAAVCCCTTCATACC 376
|||||
Db 5974 caccagagatgtgcccacagccagccctcagaccccccagctgagctcgtgattggaac 6033
|||||
Db 375 CACCAAGATGTGTGCCACAGCCAGCCCTCCAGACCCCAAGTCACTCGATGGAAAC 316
|||||
Db 6034 tcaacatcgacagcagtggtgcttgaagatgagcattagaggagccagctctga 6093
|||||
Db 315 TCACATCGCAGCAGCAGTGTGCTTTAAGAGATGCAATTAGAGGAGCCCACTGTGGA 256
|||||

Qy 6094 tctgacttgatgcccctgtggtatagcttctctgacacttggccccaatagatcc 6153
|||||
Db 255 TGTGACTTGATGATGCCCTGTGGTATCAGTCTGCTGACACTTGGCCGAATATGATCC 196
|||||
Qy 6154 agtctgacgaagcaatgtacacccgagccctcagctgagcccatctcacagtgggagca 6213
|||||
Db 195 AGTCTGAGCAAGCAATGTACACCGGAGCCTCAGTACCCATCTGCACAGTGGGAGCA 136
|||||
Qy 6214 tggagggatggtgtgctgtctctgtcttattcagctcctcagcaggaaggat 6273
|||||
Db 135 TGGAGGATGAGTGTGGCTGTGCTTATTCAGTCCCTCAGCTCAGGAGGAG 76
|||||
Qy 6274 gctagtcgtgaagtgagcctcagcagctgtgttaacttaacttattgtctacgtcca 6333
|||||
Db 75 GCTAGTCCGTAAGGTGACCTCAGACAGTACGTTAATTAACCTTATTCCTACATCTCA 16
|||||

RESULT 4
AA825207/c 508 bp mRNA EST 21-APR-1998
LOCUS oc66607.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354692 3',
DEFINITION mRNA sequence.
ACCESSION AA825207
VERSION AA825207.1 GI:2898504
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 508)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbrrp/image/image.html
Insert length: 1099 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 449.
Location/Qualifiers

FEATURES
Source 1..508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1354692"
/clone_1bp="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"

/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCTGAAGTGGAGCGCGCGCTCATTTTCTTTT-3',
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 125 a 129 c 132 g 122 t
ORIGIN

/clone="IMAGE:2087320"
 /lab_host="DHI08"
 /note="Organ: pooled: Vector: pRT3D-Pac (Pharmacia) with a modified polylinker: Site 1: Not 1: Site 2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (fetal lung NDH19W, testis NHT, and B-cell NCI-GAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 117 a 120 c 125 g 94 t
 ORIGIN

Query Match 7.0%; Score 451.8; DB 10; Length 456;
 Best Local Similarity 99.6%; Pred. No. 3.4e-45;
 Matches 453; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

5879 ccagttccctgtgctgcaagctggtgtcttctcctgtgcccctcattgtca 5938
 |||||||
 Db 456 CCACTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 397
 |||||||
 Oy 5939 tctctagatgcaactcccaatccctcattacaccacagatgtgtccagcagc 598
 |||||||
 Db 396 TCTTCAAGATGCACTCCCAATCCCTTCATACCCACAGATGTGTGCCAGCAGC 337
 |||||||
 Oy 5999 ctccagaccctcagctgcaagctgtgattggaactcaccatcgagcagctgttc 6058
 |||||||
 Db 336 CTCCAGACCCCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 277
 |||||||
 Oy 6059 tttaagagatggcattagagagagcagctcgtgagatgtgacttgatccctgtg 6118
 |||||||
 Db 276 TTTAAGAGATGCACTTAAAGAGAGCCCACTGCTGCTGCTGCTGCTGCTG 217
 |||||||
 Oy 6119 tcagctctcctgacacttgccgcaaatagatcagctgctgagcagcaaatgtacac 6178
 |||||||
 Db 216 TCACTTCTGCTACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 157
 |||||||
 Oy 6179 gagcctcaatggaccatctgacagctggtgagcattggtggttgcctgtgtc 6238
 |||||||
 Db 156 GAGCCTCAAGTGAAGCCATCTGCAAGTGGGAGCATGAGGAGATGGGCTGTGCT 97
 |||||||
 Oy 6239 tctgcttattcagctctcagctcagcaggaagatgctgctgtaagttaactaca 6298
 |||||||
 Db 96 TCTGCTTATTCAGTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 37
 |||||||
 Oy 6299 gtactgttaacttaacttattgtcactgttca 6333
 |||||||
 Db 36 GTACTGTTAATTAACTTTATGCTCACTGTCA 2

RESULT 7

LOCUS B47140 468 bp DNA GSS 21-OCT-1997
 DEFINITION HS-1068-B1-B10-MR.abi C17 Human Genomic Sperm Library C Homo
 sapiens genomic clone Plate=CT 278 COL=19 Row=D, DNA sequence.
 ACCESSION B47140
 VERSION B47140.1 GI:2551974
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 468)
 AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
 Trautcoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
 TITLE Construction of a Characterized Clone Resource for Genomic
 Sequencing: Generation and Preliminary Analysis of 20,000 Sequence

JOURNAL Tagged Connectors
 COMMENT Unpublished (1997)
 CONTACT: Mahairas GG, Zackrone KD, Hood L
 University of Washington
 Seattle, WA 98195 USA
 Tel: (206) 616-8744
 Fax: (206) 685-7301
 Email: kzackrone@u.washington.edu
 Sequence Tagged Connector
 Plate: CT 278 row: D column: 19
 Class: BAC ends
 High quality sequence stop: 468.

FEATURES
 source
 1..468
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=CT 278 COL=19 Row=D"
 /clone_lib="C17 Human Genomic Sperm Library C"
 /sex="M"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 122 a 122 c 102 g 122 t
 ORIGIN

Query Match 6.6%; Score 427.4; DB 13; Length 468;
 Best Local Similarity 99.3%; Pred. No. 2.8e-42;
 Matches 450; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Oy 1140 gccatccctctctattttgaatagattacttaataacctaattgtcactcaac 1199
 |||||||
 Db 468 GCGATCTCTCTATTTATTTGAATGATTCATTAATACACTTAATGCTACCTTCA 409
 |||||||
 Oy 1200 atcaactcaagctcgtcttttgggaacttggatcttcttttccccaatatltt 1259
 |||||||
 Db 408 ATCACTTCAAGCTCTGCTTGGGAACTTGTGGAATTTCTTTTCCCAATATTTC 349
 |||||||
 Oy 1260 taatcgaagttatgcaatctatggtggtcagatccatgaaatgagggctgtcgtga 1319
 |||||||
 Db 348 TATATCGAGATTAGTCGCAATTCATGGGTGCACTATCCATGAAATGGGGCTGCTGA 289
 |||||||
 Oy 1320 ccttagtgaatgtgtgtaaaagcatatccgatatctaaatgcatltaggtgtg 1379
 |||||||
 Db 288 CTTTATGTTAATGTTGTAATAAGCATATCCGATATTTAAATCCATTAGGCTGGGCG 229
 |||||||
 Oy 1380 cgtgtgctacgcccgtgaatccagcacttggagggcagagatgggtcttaccagat 1439
 |||||||
 Db 228 CGGTGG-TTACGCTCTGTAATCCAGCATCTTGGAGGCGGAGATGGCTTATCAGGAT 170
 |||||||
 Oy 1440 caggaatcgaacacatcctagccaacatggggaacccgctctactaataatacaaa 1499
 |||||||
 Db 169 CAGAGATCGAAGCATCTTAAGCAACATGGGGAACCCGCTCTACTAAATAATACAA 110
 |||||||
 Oy 1500 aaattgacggcggtgtgtggtgagcagcgtgtatgctcagcttaccagcttaccagcttaccag 1559
 |||||||
 Db 109 AAATTAAGCCGGGCGTGTGAGGCGGAGACCCCTGTAGTCCAGCTACTCGGAGGCTGAGCGAG 50
 |||||||
 Oy 1560 gagaatggtgtgaaccggg-gagggcgaagcttg 1591
 |||||||
 Db 49 GAGATGCGGTGAACCGGCGGAGGCGAAGCTTGG 17

RESULT 8

LOCUS AI224367 407 bp mRNA EST 21-DEC-1998
 DEFINITION GX05f07.x1 NCI-GAP_Lym12 Homo sapiens cDNA clone IMAGE:2000485 3',
 mRNA sequence.
 ACCESSION AI224367
 VERSION AI224367.1 GI:3807080
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;

REFERENCE	ATTNORS	TITLE	JOURNAL	COMMENT	FEATURES
Mammalia: Eutheria: Primates: Catarrhini: Hominoideae: Homo. 1 (bases 1 to 407)	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap.	National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Email: ccgaps-r@mail.nih.gov Unknown library type Insert Length: 675 Std Error: 0.00 Seq primer: -40UP from Glibco High quality sequence stop: 383. Location/Qualifiers 1. 407
					/organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="2000485" /clone_id="NCI-CCAP_Lym2" /tissue_type="Lymphoma, follicular mixed small and large cell" /lab_host="DH10B" /note="Organ: Lymph node; Vector: PCMV-SPORT6; Site:1: Salt; Site:2: Not; Cloned unidirectionally. Primer: 0.10g dt. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
BASE COUNT	100 a	109 c	107 g	91 t	
ORIGIN					
Query Match	6.2%	Score 403.4;	DB 10;	Length 407;	
Best Local Similarity	99.8%	Pred. No. 2,2e-39;			
Matches 404;	Conservative	0;	Mismatches 31;	Indels 0;	Gaps 0
5929	ctcatgctgattctctagatgcaatcccaatccctcatccacacagatgtgtgc	5988	ctcatgctgattctctagatgcaatcccaatccctcatccacacagatgtgtgc	5988	ctcatgctgattctctagatgcaatcccaatccctcatccacacagatgtgtgc
407	ctcatgctgattctctagatgcaatcccaatccctcatccacacagatgtgtgc	348	ctcatgctgattctctagatgcaatcccaatccctcatccacacagatgtgtgc	348	ctcatgctgattctctagatgcaatcccaatccctcatccacacagatgtgtgc
5989	ccaagcagagctccagacccccagagcgtcgtgattgtgaatccacatgcgagac	6048	ccaagcagagctccagacccccagagcgtcgtgattgtgaatccacatgcgagac	6048	ccaagcagagctccagacccccagagcgtcgtgattgtgaatccacatgcgagac
347	ccagcagagctccagacccccagagcgtcgtgattgtgaatccacatgcgagac	288	ccagcagagctccagacccccagagcgtcgtgattgtgaatccacatgcgagac	288	ccagcagagctccagacccccagagcgtcgtgattgtgaatccacatgcgagac
6049	agtggttcgatttgaagagatgagcattagagagagagccagcttgatgtgagcttgatgc	6108	agtggttcgatttgaagagatgagcattagagagagagccagcttgatgtgagcttgatgc	6108	agtggttcgatttgaagagatgagcattagagagagagccagcttgatgtgagcttgatgc
287	agtggttcgatttgaagagatgagcattagagagagagccagcttgatgtgagcttgatgc	228	agtggttcgatttgaagagatgagcattagagagagagccagcttgatgtgagcttgatgc	228	agtggttcgatttgaagagatgagcattagagagagagccagcttgatgtgagcttgatgc
6109	ccctgtggtatgagatgttcgtgcgaacatttggccgcaaatatgacagatgtgcgaagaca	6168	ccctgtggtatgagatgttcgtgcgaacatttggccgcaaatatgacagatgtgcgaagaca	6168	ccctgtggtatgagatgttcgtgcgaacatttggccgcaaatatgacagatgtgcgaagaca
227	ccctgtggtatgagatgttcgtgcgaacatttggccgcaaatatgacagatgtgcgaagaca	168	ccctgtggtatgagatgttcgtgcgaacatttggccgcaaatatgacagatgtgcgaagaca	168	ccctgtggtatgagatgttcgtgcgaacatttggccgcaaatatgacagatgtgcgaagaca
6169	atgtacacagagcagctcagatgagcccatctgtcagatgtgagagacatgagagatgtgtt	6228	atgtacacagagcagctcagatgagcccatctgtcagatgtgagagacatgagagatgtgtt	6228	atgtacacagagcagctcagatgagcccatctgtcagatgtgagagacatgagagatgtgtt
167	atgtacacagagcagctcagatgagcccatctgtcagatgtgagagacatgagagatgtgtt	108	atgtacacagagcagctcagatgagcccatctgtcagatgtgagagacatgagagatgtgtt	108	atgtacacagagcagctcagatgagcccatctgtcagatgtgagagacatgagagatgtgtt
6229	ggcctgtgctctgtcattatgaagccttcagctcagcagagagagatgtcagtcgagtaag	6288	ggcctgtgctctgtcattatgaagccttcagctcagcagagagagatgtcagtcgagtaag	6288	ggcctgtgctctgtcattatgaagccttcagctcagcagagagagatgtcagtcgagtaag
107	ggcctgtgctctgtcattatgaagccttcagctcagcagagagagatgtcagtcgagtaag	48	ggcctgtgctctgtcattatgaagccttcagctcagcagagagagatgtcagtcgagtaag	48	ggcctgtgctctgtcattatgaagccttcagctcagcagagagagatgtcagtcgagtaag
6289	tgacctacagatcgtgttaataacttatctgtcactgtcca	6333	tgacctacagatcgtgttaataacttatctgtcactgtcca	6333	tgacctacagatcgtgttaataacttatctgtcactgtcca
47	tgacctacagatcgtgttaataacttatctgtcactgtcca	3	tgacctacagatcgtgttaataacttatctgtcactgtcca	3	tgacctacagatcgtgttaataacttatctgtcactgtcca
RESULT 9					
AM292092/c	398 bp	mrna	EST	16-JAN-2000	
LOCUS					
DEFINITION	UT-H-B12-ax-a-12-0-UT. si NCI-CCAP_Sub4 Homo sapiens cDNA clone				
ACCESSION	AM292092				
VERSION	AM292092.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

	REFERENCE	Mammalia: Eutheria: Primates: Catarrhini: Homnidae; Homo.
	AUTHORS	1 (Bases 1 to 398)
	TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/ .
	JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
	COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cga@bms.femail.nih.gov The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. CGNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the: I.M.A.G.E. Consortium/LINL at: www.bio.linnl.gov/db/rp/image/image.html Seq Primer: m13 forward POLYA-yes.
FEATURES	source	Location/Qualifiers 1..398 /organism="Homo sapiens" /db_xref="taxon:9606" /clone-"IMAGE:272559" /clone_1lb="NCI_CGAP_Subd4" /lab_host="DH10B (Life Technologies)" /note="Vector: p7R73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Subd4 library is a subtracted library derived from the NCI_CGAP_Sub2 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Cc4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Cc10, NCI_CGAP_Cc16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lm2, NCI_CGAP_Pr2, NCI_CGAP_Cc8, NCI_CGAP_Cell1, NCI_CGAP_Lc12, NCI_CGAP_Br23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_Gc4, NCI_CGAP_Gc6, NCI_CGAP_Br25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_Kid3 pool 1 : LAM 3334-3337, 3682-3683, 3798-3803 (IMAGE Cloneds 1322376-1322911, 1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Cloneds 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI_CGAP_Lu5 pool 1 : LLM 3375-3582, 3851-3854 (IMAGE Cloneds 1414920-1417991, 1520904-1522439) NCI_CGAP_Gc4 pool 1 : LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE Cloneds 1257096-1258631, 1469064-1470983, 1475592-1476743)) NCI_CGAP_Pr22 pool 1 : LLM 2457-2459, 2758-2759, 3063-3068 (IMAGE Cloneds 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_Cc10 pool 1 : LLM 2644-2653, 2871-2872 (IMAGE Cloneds 1057416-1061255, 1144584-1145351)) Subtraction was performed as previously described (Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.) TAG_LIB=NCI_CGAP_Lu5 TAG_TISSUE=Lung TAG_SEQ=CACAC"
BASE COUNT	92 a 104 c 102 g 100 t	
ORIGIN		
Query Match	5.9%	Score 379.8; DB 10; Length 398;
Best Local Similarity	99.3%;	Pred. No. 1.5e-36;
Matches 381; Conservative	0; Mismatches 2;	Indels 0; Gaps 0;
OY 5951	CACCCTCAATCCCTTCATACCCAGAGGTGTGTGCCACGAGCCTCCAGACCCC	6010
Db 398	CACCTCCAAATCCCTTCATACCCAGAGGTGTGTGCCACGAGCCTCCAGACCCC	339

QY 6011 cagtgacgtcgtgattggaatacaccacgcagcagcagtggttggttaagaagatg 6070
 |||||
 Db 338 CAGTGCAGCTCGATTGTAAGAACTCACCATCGCAGGAGTGGTGGTTTAAGAGATGG 279
 QY 6071 cattagaaggagccacgtcgtgattggaatgcccgtggtatcaatttcgtg 6130
 |||||
 Db 278 CATTACAGSAGAGCCACGTCTGGATGTGGACTTGGCCCTGTGGATTCATTTGCTG 219
 QY 6131 acacttggccggaataatagatcagtgctgagcaagcaatgtacacccggaagctcagtga 6190
 |||||
 Db 218 ACACCTTGGCCGCAATAGATTCAGTCTGAGCAAGCATATACCGGAGCCTCAGTGA 159
 QY 6191 gccacatgcacagtgaggagcagatgaggtgttgccgtgtcttcctcattatca 6250
 |||||
 Db 158 GCCCATGTGACAGTGGGGACATGAGGATGGGTTTGGCCTGTCTCTCTATATCA 99
 QY 6251 gtccctcagctcaggaaggatgctagtcctgtaaggatgacctcagctactgtaatt 6310
 |||||
 Db 98 GTCCCTCAGCTCACGGAAGGATCTAGTCCGTGAAGCTCACAGTACTGTTAAT 39
 QY 6311 taacttattgtcactctcca 6333
 |||||
 Db 38 TAACTTATGTGCTCAGTCTCA 16

RESULT 10
 A1832007 376 bp mRNA EST 21-DEC-1999
 LOCUS A1832007/c w199a02.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410922 3',
 DEFINITION mRNA sequence.
 ACCESSION A1832007
 VERSION A1832007.1 GI:5452678
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 376)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrrp/image/image.html
 Insert length: 1100 Std Error: 0.00
 Seq primer: -400P from GIBCO
 High quality sequence stop: 375.
 Location/Qualifiers

FEATURES

source

1..376
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2410922"
 /clone_lib="NCI_CGAP_Lym12"
 /tissue_type="lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /note="Organ: lymph node; Vector: PCMV-SPORT6; site_1:
 SalI; site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dT. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"
 BASE COUNT 92 a 105 c 97 g 82 t
 ORIGIN

Query Match 5.8%; Score 373.4; DB 10; Length 376;
 Best Local Similarity 99.7%; Pred. No. 8.9e-36;
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5957 caatcccccataatccaccaggaatgltgtccacagcagcctccacgacccacagtc 6016
 |||||
 Db 376 CAAATCCCTCATACCCACAGAGATGTGGCCAGCCAGGCTCCAGACCCCACTGG 317
 QY 6017 agctcgtgattggaatacaccacatggcagcagcagtggttgaagaagtgcattag 6076
 |||||
 Db 316 AGCTCGTATTGGAACTCAACATCGCAGGAGTGGTGGTTTAAGAGATGATTAG 257
 QY 6077 agggagccacgtcgtgattggaatgcccgtgtggttatcaatttcgtcagcatt 6136
 |||||
 Db 256 AGGAGCCAGCTGATGTGGACTTGGATGCCCTGTGGGTATCATGTTCTGTACACTT 197
 QY 6137 tggccgaaatagatcagcagtgctgagcaagcaatgtacacccggaagctcattgagccat 6196
 |||||
 Db 196 TGCGCCGAATAGATTCAGTCTGAGCAAGCATATACCGGAGCCTCAGTGAAGCCAT 137
 QY 6197 ctgcacagtggaggacatgaggaatggtgttgccgtgtcttcctcattatcagtcctt 6256
 |||||
 Db 136 CTGCACAGTGGGACATGAGGATGGGTTTGGCCTGTCTCTTATTCAGTCCCTT 77
 QY 6257 cagctcaggaaggatgctagtcctgtaaggatgacctcagctactgtaattaaact 6316
 |||||
 Db 76 CAGTCAAGGAGGATCTAGTCCGTGAAGTACCTCACATGATTGTTAATTA 17
 QY 6317 ttattgtcactctgc 6331
 |||||
 Db 16 TTATGTCTCAGTCTG 2

RESULT 11
 A1250843 525 bp mRNA EST 21-DEC-1998
 LOCUS A1250843/c gx10a04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2000910 3',
 DEFINITION mRNA sequence.
 ACCESSION A1250843
 VERSION A1250843.1 GI:3847372
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 525)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 unknown library type
 Insert length: 1149 Std Error: 0.00
 Seq primer: -400P from GIBCO
 High quality sequence stop: 336.
 Location/Qualifiers

FEATURES

source

1..525
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2000910"
 /clone_lib="NCI_CGAP_Lym12"
 /tissue_type="lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /note="Organ: lymph node; Vector: PCMV-SPORT6; site_1:
 SalI; site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dT. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"
 BASE COUNT 143 a 141 c 136 g 104 t 1 others
 ORIGIN

Query Match 5.7%; Score 371.8; DB 10; Length 525;
 Best Local Similarity 99.2%; Pred. No. 1.2e-35;
 Matches 373; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	5956	ccaaatcccttcaatccaccacagagtgctgtgcccagccaggctctcagcaccacccagtg	6015
Db	377	CAAAATCCCTCTATTACCCACAGANNNTGTGTGCCACCCAGGCTCCACGACCCCAACTG	318
QY	6016	cagctctgtgttggaaactcaatccatctggcagcagtggttctggtttaagatgacatta	6075
Db	317	CAGCTCGGATTGTGGAAACTCAACATGCGCAGGAGTGGTTCGGTTTAAGAGATGGCATTTA	258
QY	6076	gaaggagcccaagctcgtga tggagacttgatgacgtcccttggtglatcaotltctgtacact	6135
Db	257	GAGGAGCCCAAGCTGTGATGTGGACTTGGAGGCCCTTGGGATACGTTCTGCTGACACT	198
QY	6136	ttggccccaataatagatctcagtgctcgtgagcagaatgtaaacccggagcctaagtagacca	6195
Db	197	TTGGCCCGGAATATGATCCAGTGGCTGAGCAGCAATGTACGCCGAGGCTCAGTGAACCCA	138
QY	6196	cttgcaacagtggggagcacttggaaggagttggcttggcttgcttgcctctatcagtcct	6255
Db	137	TCGTGACATGGGGAGACTGGAGAGATGGGTTTGCTGTGCTTCCTTATTCAGTCTT	78
QY	6256	tcaagctacgaaaggagatgcttagtccgtgtagagtgagcctcaagactggttcaataaac	6315
Db	77	TCAGTCACGGAAGGAGATGCTAGTCCGTGAAGGTGACCTCACAGTACTGTTAATTAAAC	18
QY	6316	tttatgtctactgtgc	6331
Db	17	TTTTATGCTACTGTC	2
RESULT	12		
A0518451			
LOCUS	A0518451	457 bp	DNA
DEFINITION	HS-5101.A2.E10.SP66 RPCT-11 Human Male BAC Library Homo sapiens	GSS	05-MAY-1999
ACCESSION	A0518451	genomic clone Plate=677 Col=20 Row=I, DNA sequence.	
VERSION	A0518451.1	GI:4743633	
KEYWORDS	GSS		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 457)		
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U. S. A.	96 (17),	9739-9744 (1999)
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallaceu.washington.edu Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPRC Resources (http://bacprc.med.buffalo.edu/ordering_bac.htm) http://www.hnsc.washington.edu Plate: 677 row: I column: 20 Seq primer: SP6 Class: BAC ends High quality sequence stop: 457. Location/Qualifiers 1..457 /organism="Homo sapiens" /db_xref="taxon:9606" /clone=Plate=677 Col=20 Row=I" /clone_lib="RPCT-11 Human Male BAC Library" /sex="male"		

BASE COUNT	78 a	133 c	129 g	115 t	2 others
ORIGIN	/Note-Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"				
Query Match	5.4%	Score 348.2	DB 13	Length 457	
Best Local Similarity	97.3%	Pred. No. 8.3e-33			
Matches	364	Conservative	0	Mismatches	9
				Indels	1
				Gaps	1
Oy	4330	taaaacatttaaccttgaccctcggagagcccaactggcatttgctgtgtgagcccaagt	4389		
Db	1	TAATAATCAATTACTCTCAACCTGACCGGACGACCAATTCCTGTGTGTCAGGCCCAATT	60		
Oy	4390	ggcaggggaacccatcacatgatgttcgcgcctctttcttgcttccttaagatgaaccag	4449		
Db	61	GGCAGGAGAACCCATATCATGATTGGCCGCTCTTCTTCTGATCCCTCATGATGAACCCAG	120		
Oy	4450	catcaagatgcactgtgtgacagatgacatgcatacccgagagatcctctcctccggaca	4509		
Db	121	CATCAAGTGCACACTGTGTGGCAGATGGCAGTGCATATACCGGAGCTACTCTCTCGGSCA	180		
Oy	4510	gattgcctctcccaagctgccgcgcgltgtgacatctatacccgagagaaatcacagac	4569		
Db	181	GATGCGCTCTCTCCACAGTCGCCGCTGTGGCACTCTACCCGAGGAGAAATACGACAGC	240		
Oy	4570	agcgcgattccagttctctggaaaatagacagacatgycacagcaagtgtgtgtgtgtctta	4629		
Db	241	ACCGGATTTCCAGTTCTGTGGAAATATACAGACATGACGACGAGCAAGTGTGGTGTCTTA	300		
Oy	4630	ggttaaaagacagacagttggccctcggtagctccgttgagccctctctctctgtgaccccttg	4689		
Db	301	TGTGAAAGCACACAGGTGGCCCTGTGTACTGGCctggc-cttctcttctgtgtccctctgc	359		
Oy	4690	cccctcttgaggctc	4703		
Db	360	CCCCNTGGGGCTTC	373		
RESULT 13					
AM003249/c	328 bp	mRNA	EST	08-MAR-2000	
LOCUS	w64a08.x1	NCI-GAP	Gc6 Homo sapiens cDNA clone IMAGE:2476070	3',	
DEFINITION	mRNA sequence.				
ACCESSION	AM003249				
VERSION	AM003249.1	GI:5850165			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
AUTHORS	Tissule: c9gabp.temall.nih.gov				
TITLE	NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.				
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
COMMENT	Unpublished (1997)				
CONTACT	Contact: Robert Strausberg, Ph.D.				
REMARKS	Tissue: c9gabp.temall.nih.gov				
REMARKS	R. Emmert-Buck, M.D., Ph.D.				
REMARKS	cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima				
REMARKS	Bonaldo, Ph.D.				
REMARKS	cDNA Library Arrayed by: Greg Lennon, Ph.D.				
REMARKS	DNA sequencing by: Washington University Genome Sequencing Center				
REMARKS	Clone distribution: NCI-GAP clone distribution information can be				
REMARKS	found through the I.M.A.G.E. Consortium/LUNL at:				
REMARKS	www.bio.liln.gov/bdnp/image/image.html				
REMARKS	Insert Length: 384 Std Error: 0.00				
REMARKS	Seq primer: -400P from Glenco.				
FEATURES	Location/Qualifiers				

source

```

1. 328
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2476070"
/clone_11b="NCI-CGAP-GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
from the normalized library NCI-CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonides
1257096-1258631, 1469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      84 a      95 c      73 g      76 t
ORIGIN

```

```

Query Match      4.7% Score 307.2; DB 10; Length 328;
Best Local Similarity 98.8%; Pred. No. 7.7e-28;
Matches 320; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```

```

QY 6011 cagtcagctcgtattggaactcaccatcgagagcaggttcgtttaaagatg 6065
DB 328 CAGTCAGCTCGTATTGGAACCTCACCTCGCAGCGCACTGTTGGTTTAAAGATG 269
QY 6070 gatttagagggagccagctctgtagtgaactgagtcctgtggtatcagttcgt 6129
DB 268 GCATTAGAGGAGCCAGCTGATGATGACTTGATGCCCTGGATATCATCTTCTGCT 209
QY 6130 gacacttggccgaaatagatcagctcgtgagaacaatgtaaccgagagctcagtg 6189
DB 208 GACACTTGGCCGAAATAGATCATGCTGAGCAACATGTACACCGAGCTCAGTG 149
QY 6190 agcccatctgcacagtgagagatgagatggtttggccctgtcttcttatttc 6249
DB 148 AGCCCATCTGCACAGTGGAGCATGAGAGATGGTTGGCCCTGTCTTCTTATTC 89
QY 6250 agtctcctagctcaggaagagatgctagctgtaagtgtagcctcacaagactggttaa 6309
DB 88 AGTCTTGAAGTCAAGAGAGGATGCTAGTCCGTGAAGTAGACCTCCAGTACTGTTAA 29
QY 6310 ttaacttatctgctcactgctca 6333
DB 28 TTAACCTTATTTGCTCACTGCTCAA 5

```

```

RESULT 14
AA825205/c 338 bp mRNA EST 21-APR-1998
LOCUS oc66e05.s1 NCI-CGAP-GC61 Homo sapiens cDNA clone IMAGE:1354688 3',
DEFINITION mRNA sequence.
ACCESSION AA825205
VERSION AA825205.1 GI:2898502
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgraphs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

```

FEATURES

source

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
 Insert length: 1077 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 135.
 Location/Qualifiers

```

1. 338
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1354688"
/clone_11b="NCI-CGAP-GC61"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - 0190 (dT) primer
[5'-TGTACCAATCTGAAGTGGAGCGCCGCTCATTTTCTTTTCTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      80 a      91 c      69 g      98 t
ORIGIN

```

```

Query Match      4.7% Score 306.8; DB 10; Length 338;
Best Local Similarity 99.4%; Pred. No. 8.5e-28;
Matches 308; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 6024 gattgaaaccacacatcgagcagtggttcgtttaaagatgcatagaggagc 6083
DB 338 GATTGAAACCTCACATCGCAGCGCATGTTGCTTTAAAGATGGATTAACGAGGAGC 279
QY 6084 caagctcgtatgtagtctgagtcctctgtggtatcagttcgtacacttggccg 6143
DB 278 CCAAGTCTGATGTGAGCTTGAGTGGCCGTGGATATCACTTCTGTACACTTTGGCCG 219
QY 6144 aaatagatcagtgctgagcaagaacatgtacacggagcctcagtgagccatcgaca 6203
DB 218 AAATAGATCCAGTGTGACAGCAAGATGTACACCGAGCTCATGAGCCATCTGCACA 159
QY 6204 gtggggagcattgagagatggtttggccctgtcttcttattcagctcagctca 6263
DB 158 GTGGGAGCATGAGAGGATGGGTGGCTGTCTCTCTCTTATTCAGTCCAGCTCA 99
QY 6264 cggagagatgtagtcgtagagtgtagcctcagtagtctgtaataacttattgc 6323
DB 98 CGGAAGGATGCTAGTCCCTGAGAGTCACTCAAGTACTGTGAATTAATTAATTATTC 39
QY 6324 tcaactgctca 6333
DB 38 TCACGTGCTCAA 29

```

```

RESULT 15
A1434322/c 315 bp mRNA EST 30-MAR-1999
LOCUS t141d01.x1 NCI-CGAP-Lym12 Homo sapiens cDNA clone IMAGE:2133025 3',
DEFINITION mRNA sequence.
ACCESSION A1434322
VERSION A1434322.1 GI:4295368
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

```

REFERENCE 1 (bases 1 to 315)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
www-bio.lnl.gov/bbrp/image/image.html
 Insert length: 1751 Std Error: 0.00
 Seq primer: -400P from Glibco
 High quality sequence stop: 308.
 Location/Qualifiers

FEATURES

source 1..315
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2133025"
 /clone_lib="NCI-CGAP_Lym12"
 /tissue_type="Lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /note="Organ: lymph node; Vector: PCMV-SPORT6; Site_1:
 Salt: Site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dt: Average insert size 1.25 Kb. Life Technologies
 catalog #: 11547-015"
 BASE COUNT 82 a 94 c 70 g 69 t
 ORIGIN

Query Match 4.7%; Score 304; DB 10; Length 315;
 Best local Similarity 99.7%; Pred. No. 1.9e-27;

Matches 315; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 6016 caacttgatggaactcaccatcgagcagctggttcggttaagatgaccta 6075
 |||||||
 DB 315 CAGCTGTAATTGGAACCT-ACCATGGCAGGACAGTGTTCGTTTAAGATGCACTTA 257
 |||||||
 QY 6076 gaaggagccagctgagatgagacttgatgacccctggtgtatcaagttctgcgaact 6135
 |||||||
 DB 256 GAGGAGAGCCAGCTCGATGTGACTGTGATGCCCTGTGGTATCATGTCGTGACACT 197
 |||||||
 QY 6136 ttgagccgaataatagatcagctgctgagcaagcaatgtacacccgagcctcagtgagccca 6195
 |||||||
 DB 196 TTGGCCCGAAATAGATCAGTCTGCTAGCAAGCATGTACACCGAGCCTCAGTGAGCCCA 137
 |||||||
 QY 6196 tctgacagtgaggagcatggaagatggttggcctgtgcttgccttattcaatcct 6255
 |||||||
 DB 136 TCTGCACAGTGGGAGCATGAGGATGGGTTTGCCCTGTGCTTCTGCTATTCAGTCTT 77
 |||||||
 QY 6256 tcagctcaggaagagatgctagtcctgtaagagtgacctcacagtaactgtaataaac 6315
 |||||||
 DB 76 TCAGCTCAGGAGAGGAGATGCTAGTCCGTGAAGTGACCTCACAGTACTGTTAATTAAC 17
 |||||||
 QY 6316 ttattgtcactgtc 6331
 |||||||
 DB 16 TTTATTGCTCACTGTC 1

Search completed: November 29, 2001, 05:50:11
 Job time: 6357 sec